SEQUENCE LISTING

<110> Edgar B. Cahoon
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Charles W. Kolar
Zhan Bin Liu

<120> Production of Long Chain Polyunsaturated Fatty Acids in Plants

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<150> US 60/446,941
<151> 2003-02-12

<160> 98

<170> PatentIn version 3.2

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245 250 255

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Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
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Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
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Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys
115 120 125

Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu
130 135 140

His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly
145 150 155 160

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Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val
180 185 190

Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His
195 200 205

Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala
210 215 220

Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser
225 230 235 240

Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe
245 250 255

Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg
260 265 270

```
Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly
        275                 280                 285

Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala
    290                 295                 300

Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala
305                 310                 315                 320

Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala
                325                 330                 335

Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly
            340                 345                 350
Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln
        355                 360                 365

Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe
    370                 375                 380

Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val
385                 390                 395                 400

Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys
                405                 410                 415

Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met
            420                 425                 430

Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys
        435                 440                 445

Glu Phe Pro Ala Met
    450
```

<210> 37
<211> 1413
<212> DNA
<213> Saprolegnia diclina

<400> 37

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atggccccgc agacggagct ccgccagcgc cacgccgccg tcgccgagac gccggtggcc     60
ggcaagaagg cctttacatg gcaggaggtc gcgcagcaca acacggcggc ctcggcctgg    120
atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc    180
cgcgagatgg tgctgctgca cgccggtcgc gaggccaccg acacgttcga ctcgtaccac    240
ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agattggcac gttcacgggc    300
ccgtccgagt ttccgacctt caagccggac acgggcttct acaaggagtg ccgcaagcgc    360
gttggcgagt acttcaagaa gaacaacctc catccgcagg acggcttccc gggcctctgg    420
cgcatgatgg tcgtgtttgc ggtcgccggc ctcgccttgt acggcatgca cttttcgact    480
atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgctg    540
ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatgccgtt cttccattac    600
gtcgtcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac    660
cagcacgtcg tgggccacca catctacacg aacgtcgcgg gctcggaccc ggatcttccg    720
gtcaacatgg acggcgacat ccgccgcatc gtgaaccgcc aggtgttcca gcccatgtac    780
gcattccagc acatctacct tccgccgctc tatggcgtgc ttggcctcaa gttccgcatc    840
caggacttca ccgacacgtt cggctcgcac acgaacggcc cgatccgcgt caacccgcac    900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg    960
taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttcctc   1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc   1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc   1140
```

```
tcgcaggtca agacgtcggt cgactacgcc catggctcgt ggatgacgac gttccttgcc   1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac   1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc   1320
ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catgggccag   1380
cagggcatcg ccgccacgat ccacatgggc taa                                1413
```

<210> 38
<211> 470
<212> PRT
<213> Saprolegnia diclina

<400> 38

```
Met Ala Pro Gln Thr Glu Leu Arg Gln Arg His Ala Ala Val Ala Glu
1               5                  10                  15

Thr Pro Val Ala Gly Lys Lys Ala Phe Thr Trp Gln Glu Val Ala Gln
            20                  25                  30

His Asn Thr Ala Ala Ser Ala Trp Ile Ile Ile Arg Gly Lys Val Tyr
        35                  40                  45

Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val
    50                  55                  60

Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His
65                  70                  75                  80

Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly
                85                  90                  95

Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly
            100                 105                 110

Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn
        115                 120                 125

Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val
    130                 135                 140

Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr
145                 150                 155                 160

Ile Phe Ala Leu Gln Leu Ala Ala Ala Ala Leu Phe Gly Val Cys Gln
                165                 170                 175

Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr
            180                 185                 190

Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp
        195                 200                 205

Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val
    210                 215                 220

Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro
225                 230                 235                 240

Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe
                245                 250                 255
```

```
Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly
            260                 265                 270

Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly
        275                 280                 285

Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr
    290                 295                 300

Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val
305                 310                 315                 320

Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala
                325                 330                 335

Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn
            340                 345                 350

Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp
        355                 360                 365

Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys
    370                 375                 380

Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met Thr Thr Phe Leu Ala
385                 390                 395                 400

Gly Ala Leu Asn Tyr Gln Val Val His His Leu Phe Pro Ser Val Ser
                405                 410                 415

Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys
            420                 425                 430

Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe
        435                 440                 445

Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala
    450                 455                 460

Ala Thr Ile His Met Gly
465                 470
```

<210> 39
<211> 819
<212> DNA
<213> Thraustochytrium aureum

<400> 39

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atggcaaaca gcagcgtgtg ggatgatgtg gtgggccgcg tggagaccgg cgtggaccag     60
tggatggatg gcgccaagcc gtacgcactc accgatgggc tcccgatgat ggacgtgtcc    120
accatgctgg cattcgaggt gggatacatg gccatgctgc tcttcggcat cccgatcatg    180
aggcagatgg agaagccttt tgagctcaag accatcaagc tcttgcacaa cttgtttctc    240
ttcggacttt ccttgtacat gtgcgtggtg accatccgcc aggctatcct tggaggctac    300
aaagtgtttg gaaacgacat ggagaagggc aacgagtctc atgctcaggg catgtctcgc    360
atcgtgtacg tgttctacgt gtccaaggca tacgagttct tggataccgc catcatgatc    420
ctttgcaaga agttcaacca ggtttccttc ttgcatgtgt accaccatgc caccattttt    480
gccatctggt gggctatcgc caagtacgct ccaggaggtg atgcgtactt ttcagtgatc    540
ctcaactctt tcgtgcacac cgtcatgtac gcatactact tcttctcctc ccaagggttc    600
gggttcgtga agccaatcaa gccgtacatc accacccttc agatgaccca gttcatggca    660
atgcttgtgc agtccttgta cgactacctc ttcccatgcg actacccaca ggctcttgtg    720
```

cagcttcttg gagtgtacat gatcaccttg cttgccctct tcggcaactt ttttgtgcag 780
agctatctta aaaagccaaa aaagagcaag accaactaa 819

<210> 40
<211> 272
<212> PRT
<213> Thraustochytrium aureum

<400> 40
Met Ala Asn Ser Ser Val Trp Asp Asp Val Val Gly Arg Val Glu Thr
1 5 10 15

Gly Val Asp Gln Trp Met Asp Gly Ala Lys Pro Tyr Ala Leu Thr Asp
20 25 30

Gly Leu Pro Met Met Asp Val Ser Thr Met Leu Ala Phe Glu Val Gly
35 40 45

Tyr Met Ala Met Leu Leu Phe Gly Ile Pro Ile Met Arg Gln Met Glu
50 55 60

Lys Pro Phe Glu Leu Lys Thr Ile Lys Leu Leu His Asn Leu Phe Leu
65 70 75 80

Phe Gly Leu Ser Leu Tyr Met Cys Val Val Thr Ile Arg Gln Ala Ile
85 90 95

Leu Gly Gly Tyr Lys Val Phe Gly Asn Asp Met Glu Lys Gly Asn Glu
100 105 110

Ser His Ala Gln Gly Met Ser Arg Ile Val Tyr Val Phe Tyr Val Ser
115 120 125

Lys Ala Tyr Glu Phe Leu Asp Thr Ala Ile Met Ile Leu Cys Lys Lys
130 135 140

Phe Asn Gln Val Ser Phe Leu His Val Tyr His His Ala Thr Ile Phe
145 150 155 160

Ala Ile Trp Trp Ala Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr
165 170 175

Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr
180 185 190

Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro
195 200 205

Tyr Ile Thr Thr Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln
210 215 220

Ser Leu Tyr Asp Tyr Leu Phe Pro Cys Asp Tyr Pro Gln Ala Leu Val
225 230 235 240

Gln Leu Leu Gly Val Tyr Met Ile Thr Leu Leu Ala Leu Phe Gly Asn
245 250 255

Phe Phe Val Gln Ser Tyr Leu Lys Lys Pro Lys Lys Ser Lys Thr Asn
260 265 270

<210> 41
<211> 1077
<212> DNA
<213> Saprolegnia diclina

<400> 41
atgactgagg ataagacgaa ggtcgagttc ccgacgctca cggagctcaa gcactcgatc 60
ccgaacgcgt gctttgagtc gaacctcggc ctctcgctct actacacggc ccgcgcgatc 120
ttcaacgcgt cggcctcggc ggcgctgctc tacgcggcgc gctcgacgcc gttcattgcc 180
gataacgttc tgctccacgc gctcgtttgc gccacctaca tctacgtgca gggcgtcatc 240
ttctggggct tcttcacggt cggccacgac tgcggccact cggccttctc gcgctaccac 300
agcgtcaact ttatcatcgg ctgcatcatg cactctgcga ttttgacgcc gttcgagagc 360
tggcgcgtga cgcaccgcca ccaccacaag aacacgggca acattgataa ggacgagatc 420
ttttacccgc accggtcggt caaggacctc caggacgtgc gccaatgggt ctacacgctc 480
ggcggtgcgt ggtttgtcta cttgaaggtc gggtatgccc cgcgcacgat gagccacttt 540
gacccgtggg acccgctcct ccttcgccgc gcgtcggccg tcatcgtgtc gctcggcgtc 600
tgggccgcct tcttcgccgc gtacgcgtac ctcacatact cgctcggctt tgccgtcatg 660
ggcctctact actatgcgcc gctctttgtc tttgcttcgt tcctcgtcat tacgaccttc 720
ttgcaccaca acgacgaagc gacgccgtgg tacggcgact cggagtggac gtacgtcaag 780
ggcaacctct cgagcgtcga ccgctcgtac ggcgcgttcg tggacaacct gagccaccac 840
attggcacgc accaggtcca ccacttgttc ccgatcattc cgcactacaa gctcaacgaa 900
gccaccaagc actttgcggc cgcgtacccg cacctcgtgc gcaggaacga cgagcccatc 960
atcacggcct tcttcaagac cgcgcacctc tttgtcaact acggcgctgt gcccgagacg 1020
gcgcagatct tcacgctcaa agagtcggcc gcggccgcca aggccaagtc ggactaa 1077

<210> 42
<211> 358
<212> PRT
<213> Saprolegnia diclina

<400> 42
Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
1 5 10 15

Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
20 25 30

Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
35 40 45

Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
50 55 60

Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
65 70 75 80

Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
85 90 95

Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
100 105 110

Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
115 120 125

His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
130 135 140

Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145 150 155 160

```
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
                165                 170                 175

Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
            180                 185                 190

Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
        195                 200                 205

Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
    210                 215                 220

Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225                 230                 235                 240

Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
                245                 250                 255

Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
            260                 265                 270

Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
        275                 280                 285

Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
    290                 295                 300

Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305                 310                 315                 320

Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
                325                 330                 335

Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
            340                 345                 350

Ala Lys Ala Lys Ser Asp
        355
```

<210> 43
<211> 957
<212> DNA
<213> Mortierella alpina

<400> 43

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atggagtcga ttgcgccatt cctcccatca aagatgccgc aagatctgtt tatggacctt     60
gccaccgcta tcggtgtccg ggccgcgccc tatgtcgatc ctctcgaggc cgcgctggtg    120
gcccaggccg agaagtacat ccccacgatt gtccatcaca cgcgtgggtt cctggtcgcg    180
gtggagtcgc ctttggcccg tgagctgccg ttgatgaacc cgttccacgt gctgttgatc    240
gtgctcgctt atttggtcac ggtctttgtg ggcatgcaga tcatgaagaa ctttgagcgg    300
ttcgaggtca agacgttttc gctcctgcac aacttttgtc tggtctcgat cagcgcctac    360
atgtgcggtg ggatcctgta cgaggcttat caggccaact atggactgtt tgagaacgct    420
gctgatcata ccttcaaggg tcttcctatg gccaagatga tctggctctt ctacttctcc    480
aagatcatgg agtttgtcga caccatgatc atggtcctca agaagaacaa ccgccagatc    540
tccttcttgc acgtttacca ccacagctcc atcttcacca tctggtggtt ggtcaccttt    600
gttgcaccca acggtgaagc ctacttctct gctgcgttga actcgttcat ccatgtgatc    660
atgtacggct actacttctt gtcggccttg ggcttcaagc aggtgtcgtt catcaagttc    720
tacatcacgc gctcgcagat gacacagttc tgcatgatgt cggtccagtc ttcctgggac    780
atgtacgcca tgaaggtcct tggccgcccc ggataccct tcttcatcac ggctctgctt    840
```

tggttctaca tgtggaccat gctcggtctc ttctacaact tttacagaaa gaacgccaag 900
ttggccaagc aggccaaggc cgacgctgcc aaggagaagg caaggaagtt gcagtaa 957

<210> 44
<211> 318
<212> PRT
<213> Mortierella alpina

<400> 44

```
Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu
1               5                  10                  15

Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val
            20                  25                  30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro
        35                  40                  45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro
    50                  55                  60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile
65                  70                  75                  80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys
                85                  90                  95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe
            100                 105                 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu
        115                 120                 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr
    130                 135                 140

Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser
145                 150                 155                 160

Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn
                165                 170                 175

Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe
            180                 185                 190

Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr
        195                 200                 205

Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr
    210                 215                 220

Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe
225                 230                 235                 240

Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln
                245                 250                 255

Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr
            260                 265                 270
```

```
Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu
        275                 280                 285

Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln
    290                 295                 300

Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln
305                 310                 315
```

<210> 45
<211> 1483
<212> DNA
<213> Mortierella alpina

<400> 45

```
gcttcctcca gttcatcctc catttcgcca cctgcattct ttacgaccgt taagcaagat     60
gggaacggac caaggaaaaa ccttcacctg ggaagagctg gcggcccata acaccaagga    120
cgacctactc ttggccatcc gcggcagggt gtacgatgtc acaaagttct tgagccgcca    180
tcctggtgga gtggacactc tcctgctcgg agctggccga gatgttactc cggtctttga    240
gatgtatcac gcgtttgggg ctgcagatgc cattatgaag aagtactatg tcggtacact    300
ggtctcgaat gagctgccca tcttcccgga gccaacggtg ttccacaaaa ccatcaagac    360
gagagtcgag ggctacttta cggatcggaa cattgatccc aagaatagac cagagatctg    420
gggacgatac gctcttatct ttggatcctt gatcgcttcc tactacgcgc agctctttgt    480
gcctttcgtt gtcgaacgca catggcttca ggtggtgttt gcaatcatca tgggatttgc    540
gtgcgcacaa gtcggactca accctcttca tgatgcgtct cacttttcag tgacccacaa    600
ccccactgtc tggaagattc tgggagccac gcacgacttt ttcaacggag catcgtacct    660
ggtgtggatg taccaacata tgctcggcca tcacccctac accaacattg ctggagcaga    720
tcccgacgtg tcgacgtctg agcccgatgt tcgtcgtatc aagcccaacc aaaagtggtt    780
tgtcaaccac atcaaccagc acatgtttgt tcctttcctg tacggactgc tggcgttcaa    840
ggtgcgcatt caggacatca acattttgta ctttgtcaag accaatgacg ctattcgtgt    900
caatcccatc tcgacatggc acactgtgat gttctggggc ggcaaggctt tctttgtctg    960
gtatcgcctg attgttcccc tgcagtatct gcccctgggc aaggtgctgc tcttgttcac   1020
ggtcgcggac atggtgtcgt cttactggct ggcgctgacc ttccaggcga accacgttgt   1080
tgaggaagtt cagtggccgt tgcctgacga gaacgggatc atccaaaagg actgggcagc   1140
tatgcaggtc gagactacgc aggattacgc acacgattcg cacctctgga ccagcatcac   1200
tggcagcttg aactaccagg ctgtgcacca tctgttcccc aacgtgtcgc agcaccatta   1260
tcccgatatt ctggccatca tcaagaacac ctgcagcgag tacaaggttc cataccttgt   1320
caaggatacg ttttggcaag catttgcttc acatttggag cacttgcgtg ttcttggact   1380
ccgtcccaag gaagagtaga agaaaaaaag cgccgaatga agtattgccc ccttttttctc   1440
caagaatggc aaaaggagat caagtggaca ttctctatga aga                      1483
```

<210> 46
<211> 446
<212> PRT
<213> Mortierella alpina

<400> 46

```
Met Gly Thr Asp Gln Gly Lys Thr Phe Thr Trp Glu Glu Leu Ala Ala
1               5                   10                  15

His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr
            20                  25                  30

Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu
        35                  40                  45

Leu Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His
    50                  55                  60
```

```
Ala Phe Gly Ala Ala Asp Ala Ile Met Lys Lys Tyr Tyr Val Gly Thr
65                  70                  75                  80

Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His
                85                  90                  95

Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile
            100                 105                 110

Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe
        115                 120                 125

Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Pro Phe Val
    130                 135                 140

Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Ile Met Gly Phe
145                 150                 155                 160

Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe
                165                 170                 175

Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His
            180                 185                 190

Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met
        195                 200                 205

Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val
    210                 215                 220

Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp
225                 230                 235                 240

Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly
                245                 250                 255

Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe
            260                 265                 270

Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His
        275                 280                 285

Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu
    290                 295                 300

Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe
305                 310                 315                 320

Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln
                325                 330                 335

Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn
            340                 345                 350

Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln
        355                 360                 365

Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu
    370                 375                 380
```

```
Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His
385                 390                 395                 400

Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys
                405                 410                 415

Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His
            420                 425                 430

Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu
        435                 440                 445
```

<210> 47
<211> 1350
<212> DNA
<213> Arabidopsis thaliana

<400> 47

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ctctctctct ctctcttctc tctttctctc cccctctctc cggcgatggt tgttgctatg     60
gaccaacgca ccaatgtgaa cggagatccc ggcgccggag accggaagaa agaagaaagg    120
tttgatccga gtgcacaacc accgttcaag atcggagata taagggcggc gattcctaag    180
cactgttggg ttaagagtcc tttgagatca atgagttacg tcgtcagaga cattatcgcc    240
gtcgcggctt tggccatcgc tgccgtgtat gttgatagct ggttcctttg gcctctttat    300
tgggccgccc aaggaacact tttctgggcc atctttgttc tcggccacga ctgtggacat    360
gggagtttct cagacattcc tctactgaat agtgtggttg gtcacattct tcattctttc    420
atcctcgttc cttaccatgg ttggagaata agccaccgga cacaccacca gaaccatggc    480
catgttgaaa acgacgagtc atgggttccg ttaccagaaa gggtgtacaa gaaattgccc    540
cacagtactc ggatgctcag atacactgtc cctctcccca tgctcgcata tcctctctat    600
ttgtgctaca gaagtcctgg aaaagaagga tcacatttta acccatacag tagtttattt    660
gctccaagcg agagaaagct tattgcaact tcaactactt gttggtccat aatgttcgtc    720
agtcttatcg ctctatcttt cgtcttcggt ccactcgcgg ttcttaaagt ctacggtgta    780
ccgtacatta tctttgtgat gtggttggat gctgtcacgt atttgcatca tcatggtcac    840
gatgagaagt tgccttggta tagaggcaag gaatggagtt atctacgtgg aggattaaca    900
acaattgata gagattacgg aatctttaac aacattcatc acgacattgg aactcacgtg    960
atccatcatc tcttcccaca aatccctcac tatcacttgg tcgacgccac gaaagcagct   1020
aaacatgtgt tgggaagata ctacagagaa ccaaagacgt caggagcaat accgatccac   1080
ttggtggaga gtttggtcgc aagtattaag aaagatcatt acgtcagcga cactggtgat   1140
attgtcttct acgagacaga tccagatctc tacgtttacg cttctgacaa atctaaaatc   1200
aattaatctc catttgttta gctctattag gaataaacca gcccactttt aaaatttta    1260
tttcttgttg tttttaagtt aaaagtgtac tcgtgaaact ctttttttt tctttttttt    1320
tattaatgta tttacattac aaggcgtaaa                                    1350
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<210> 48
<211> 386
<212> PRT
<213> Arabidopsis thaliana

<400> 48

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Met Val Val Ala Met Asp Gln Arg Thr Asn Val Asn Gly Asp Pro Gly
1               5                   10                  15

Ala Gly Asp Arg Lys Lys Glu Glu Arg Phe Asp Pro Ser Ala Gln Pro
            20                  25                  30

Pro Phe Lys Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp
        35                  40                  45

Val Lys Ser Pro Leu Arg Ser Met Ser Tyr Val Val Arg Asp Ile Ile
    50                  55                  60
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Ala Val Ala Ala Leu Ala Ile Ala Ala Val Tyr Val Asp Ser Trp Phe
65                  70                  75                  80

Leu Trp Pro Leu Tyr Trp Ala Ala Gln Gly Thr Leu Phe Trp Ala Ile
                85                  90                  95

Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro
            100                 105                 110

Leu Leu Asn Ser Val Val Gly His Ile Leu His Ser Phe Ile Leu Val
        115                 120                 125

Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His
    130                 135                 140

Gly His Val Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Arg Val
145                 150                 155                 160

Tyr Lys Lys Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro
                165                 170                 175

Leu Pro Met Leu Ala Tyr Pro Leu Tyr Leu Cys Tyr Arg Ser Pro Gly
            180                 185                 190

Lys Glu Gly Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser
        195                 200                 205

Glu Arg Lys Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Phe
    210                 215                 220

Val Ser Leu Ile Ala Leu Ser Phe Val Phe Gly Pro Leu Ala Val Leu
225                 230                 235                 240

Lys Val Tyr Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala
                245                 250                 255

Val Thr Tyr Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr
            260                 265                 270

Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp
        275                 280                 285

Arg Asp Tyr Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His
    290                 295                 300

Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp
305                 310                 315                 320

Ala Thr Lys Ala Ala Lys His Val Leu Gly Arg Tyr Tyr Arg Glu Pro
                325                 330                 335

Lys Thr Ser Gly Ala Ile Pro Ile His Leu Val Glu Ser Leu Val Ala
            340                 345                 350

Ser Ile Lys Lys Asp His Tyr Val Ser Asp Thr Gly Asp Ile Val Phe
        355                 360                 365

Tyr Glu Thr Asp Pro Asp Leu Tyr Val Tyr Ala Ser Asp Lys Ser Lys
    370                 375                 380
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Ile Asn
385

<210> 49
<211> 834
<212> DNA
<213> Pavlova sp.

<400> 49
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gacattgaca accccaacgg ggcctactcg acctcgtgga ctggcctgcc cattgtgatg 120
tctgtggtct atctcagcgg tgtgtttggg ctcacaaagt acttcgagaa ccggaagccc 180
atgacggggc tgaaggacta catgttcact tacaatctct accaggtgat catcaacgtg 240
tggtgcgtgg tggcctttct cctggaggtg cggcgtgcgg gcatgtcact catcggcaat 300
aaggtggacc ttgggcccaa ctccttcagg ctcggcttcg tcacgtgggt gcactacaac 360
aacaagtacg tggagctcct cgacacccta tggatggtgc tgcgcaagaa gacgcagcag 420
gtctccttcc tccacgtcta tcatcacgtg cttctgatgt gggcctggtt cgttgtcgtc 480
aagctcggca atggtggtga cgcatatttt ggcggtctca tgaactcgat catccacgtg 540
atgatgtatt cctactacac catggcgctc ctgggctggt catgcccctg gaagcgctac 600
ctcacgcagg cacagctcgt gcagttttgc atctgcctcg cccactccac atgggcggca 660
gtaacgggtg cctacccgtg gcgaatttgc ttggtggagg tgtgggtgat ggtgtccatg 720
ctggtgctct tcacacgctt ctaccgccag gcctatgcca aggaggcgaa ggccaaggag 780
gcgaaaaagc tcgcacagga ggcatcacag gccaaggcgg tcaaggcgga gtaa 834

<210> 50
<211> 277
<212> PRT
<213> Pavlova sp.

<400> 50
Met Met Leu Ala Ala Gly Tyr Leu Leu Val Leu Ser Ala Ala Arg Gln
1 5 10 15

Ser Phe Gln Gln Asp Ile Asp Asn Pro Asn Gly Ala Tyr Ser Thr Ser
20 25 30

Trp Thr Gly Leu Pro Ile Val Met Ser Val Val Tyr Leu Ser Gly Val
35 40 45

Phe Gly Leu Thr Lys Tyr Phe Glu Asn Arg Lys Pro Met Thr Gly Leu
50 55 60

Lys Asp Tyr Met Phe Thr Tyr Asn Leu Tyr Gln Val Ile Ile Asn Val
65 70 75 80

Trp Cys Val Val Ala Phe Leu Leu Glu Val Arg Arg Ala Gly Met Ser
85 90 95

Leu Ile Gly Asn Lys Val Asp Leu Gly Pro Asn Ser Phe Arg Leu Gly
100 105 110

Phe Val Thr Trp Val His Tyr Asn Asn Lys Tyr Val Glu Leu Leu Asp
115 120 125

Thr Leu Trp Met Val Leu Arg Lys Lys Thr Gln Gln Val Ser Phe Leu
130 135 140

His Val Tyr His His Val Leu Leu Met Trp Ala Trp Phe Val Val Val
145 150 155 160

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Lys Leu Gly Asn Gly Gly Asp Ala Tyr Phe Gly Gly Leu Met Asn Ser
                165                 170                 175

Ile Ile His Val Met Met Tyr Ser Tyr Tyr Thr Met Ala Leu Leu Gly
            180                 185                 190

Trp Ser Cys Pro Trp Lys Arg Tyr Leu Thr Gln Ala Gln Leu Val Gln
        195                 200                 205

Phe Cys Ile Cys Leu Ala His Ser Thr Trp Ala Ala Val Thr Gly Ala
    210                 215                 220

Tyr Pro Trp Arg Ile Cys Leu Val Glu Val Trp Val Met Val Ser Met
225                 230                 235                 240

Leu Val Leu Phe Thr Arg Phe Tyr Arg Gln Ala Tyr Ala Lys Glu Ala
                245                 250                 255

Lys Ala Lys Glu Ala Lys Lys Leu Ala Gln Glu Ala Ser Gln Ala Lys
            260                 265                 270

Ala Val Lys Ala Glu
        275
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<210> 51
<211> 1530
<212> DNA
<213> Schizochytrium aggregatum

<400> 51

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atgacggtgg gcggcgatga ggtgtacagc atggcgcagg tgcgcgacca caacaccccg     60
gacgacgcct ggtgcgccat ccacggcgag gtgtacgagc tgaccaagtt cgcccgcacc    120
caccccgggg gggacatcat cttgctggcc gccggcaagg aggccaccat cctgttcgag    180
acgtaccacg tgcgccccat ctccgacgcg gtcctgcgca agtaccgcat cggcaagctc    240
gccgccgccg gcaaggatga gccggccaac gacagcacct actacagctg ggacagcgac    300
ttttacaagg tgctccgcca gcgtgtcgtg gcgcgcctcg aggagcgcaa gatcgcccgc    360
cgcggcggcc ccgagatctg gatcaaggcc gccatcctcg tcagcggctt ctggtccatg    420
ctctacctca tgtgcaccct ggacccgaac cgcggcgcca tcctggccgc catcgcgctg    480
ggcatcgtcg ccgccttcgt cggcacgtgc attcagcacg acggcaacca cggcgcgttc    540
gccttctctc cgttcatgaa caagctctct ggctggacgc tcgacatgat cggcgccagt    600
gccatgacct gggagatgca gcacgtgctg ggccaccacc cgtacaccaa cctgatcgag    660
atggagaacg gcacccaaaa ggtcacccac gccgacgtcg accccaagaa ggccgaccag    720
gagagcgacc cggacgtctt cagcacctac cccatgctcc gtctgcaccc gtggcaccgc    780
aagcgcttct accaccgctt ccagcacctg tacgcgccgc tgctcttcgg tttcatgacc    840
atcaacaagg tgatcaccca ggatgtggga gttgtcctca gcaagcgtct gtttcagatc    900
gatgccaact gccgttacgc cagcaagtcg tacgttgcgc gcttctggat catgaagctg    960
ctcaccgtcc tctacatggt cgccctcccc gtgtacaccc agggccttgt cgacgggctc   1020
aagctcttct tcatcgccca cttttcgtgc ggcgagctgc tggccaccat gttcatcgtc   1080
aaccacatca tcgagggcgt ctcgtacgcc tccaaggact ctgtcaaggg caccatggcg   1140
ccgccgcgca cggtgcacgg cgtgaccccg atgcatgaca cccgcgacgc gctcggcaag   1200
gagaaggcag ccaccaagca cgtgccgctc aacgactggg ccgcggtcca gtgccagacc   1260
tcggtcaact ggtcgatcgg ctcgtggttc tggaaccact tctccggcgg gctcaaccac   1320
cagatcgagc accacctctt ccccggcctc acccacacca cctacgtgta cattcaggat   1380
gtggtgcagg cgacgtgcgc cgagtacggg gtcccgtacc agtcggagca gagcctcttc   1440
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tgggagaagg accaccccaa gtccaagtga                                    1530
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<210> 52
<211> 509

<212> PRT
<213> Schizochytrium aggregatum

<400> 52

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Met Thr Val Gly Gly Asp Glu Val Tyr Ser Met Ala Gln Val Arg Asp
1               5                  10                  15

His Asn Thr Pro Asp Asp Ala Trp Cys Ala Ile His Gly Glu Val Tyr
            20                  25                  30

Glu Leu Thr Lys Phe Ala Arg Thr His Pro Gly Gly Asp Ile Ile Leu
        35                  40                  45

Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Val
    50                  55                  60

Arg Pro Ile Ser Asp Ala Val Leu Arg Lys Tyr Arg Ile Gly Lys Leu
65                  70                  75                  80

Ala Ala Ala Gly Lys Asp Glu Pro Ala Asn Asp Ser Thr Tyr Tyr Ser
                85                  90                  95

Trp Asp Ser Asp Phe Tyr Lys Val Leu Arg Gln Arg Val Val Ala Arg
            100                 105                 110

Leu Glu Glu Arg Lys Ile Ala Arg Arg Gly Gly Pro Glu Ile Trp Ile
        115                 120                 125

Lys Ala Ala Ile Leu Val Ser Gly Phe Trp Ser Met Leu Tyr Leu Met
    130                 135                 140

Cys Thr Leu Asp Pro Asn Arg Gly Ala Ile Leu Ala Ala Ile Ala Leu
145                 150                 155                 160

Gly Ile Val Ala Ala Phe Val Gly Thr Cys Ile Gln His Asp Gly Asn
                165                 170                 175

His Gly Ala Phe Ala Phe Ser Pro Phe Met Asn Lys Leu Ser Gly Trp
            180                 185                 190

Thr Leu Asp Met Ile Gly Ala Ser Ala Met Thr Trp Glu Met Gln His
        195                 200                 205

Val Leu Gly His His Pro Tyr Thr Asn Leu Ile Glu Met Glu Asn Gly
    210                 215                 220

Thr Gln Lys Val Thr His Ala Asp Val Asp Pro Lys Lys Ala Asp Gln
225                 230                 235                 240

Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr Pro Met Leu Arg Leu His
                245                 250                 255

Pro Trp His Arg Lys Arg Phe Tyr His Arg Phe Gln His Leu Tyr Ala
            260                 265                 270

Pro Leu Leu Phe Gly Phe Met Thr Ile Asn Lys Val Ile Thr Gln Asp
        275                 280                 285

Val Gly Val Val Leu Ser Lys Arg Leu Phe Gln Ile Asp Ala Asn Cys
    290                 295                 300
```

```
Arg Tyr Ala Ser Lys Ser Tyr Val Ala Arg Phe Trp Ile Met Lys Leu
305                 310                 315                 320

Leu Thr Val Leu Tyr Met Val Ala Leu Pro Val Tyr Thr Gln Gly Leu
                325                 330                 335

Val Asp Gly Leu Lys Leu Phe Phe Ile Ala His Phe Ser Cys Gly Glu
            340                 345                 350

Leu Leu Ala Thr Met Phe Ile Val Asn His Ile Ile Glu Gly Val Ser
        355                 360                 365

Tyr Ala Ser Lys Asp Ser Val Lys Gly Thr Met Ala Pro Pro Arg Thr
    370                 375                 380

Val His Gly Val Thr Pro Met His Asp Thr Arg Asp Ala Leu Gly Lys
385                 390                 395                 400

Glu Lys Ala Ala Thr Lys His Val Pro Leu Asn Asp Trp Ala Ala Val
                405                 410                 415

Gln Cys Gln Thr Ser Val Asn Trp Ser Ile Gly Ser Trp Phe Trp Asn
            420                 425                 430

His Phe Ser Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro
        435                 440                 445

Gly Leu Thr His Thr Thr Tyr Val Tyr Ile Gln Asp Val Val Gln Ala
    450                 455                 460

Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu Gln Ser Leu Phe
465                 470                 475                 480

Ser Ala Tyr Phe Lys Met Leu Ser His Leu Arg Ala Leu Gly Asn Glu
                485                 490                 495

Pro Met Pro Ser Trp Glu Lys Asp His Pro Lys Ser Lys
            500                 505
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<210> 53
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 53
gcggccgcat gactgaggat aagacga 27

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 54
gcggccgctt agtccgactt ggccttg 27

<210> 55
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 55
gcggccgcat ggagtcgatt gcgc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 56
gcggccgctt actgcaactt cctt 24

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 57
gcggccgcat gggaacggac caag 24

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 58
gcggccgcct actcttcctt ggga 24

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 59
ttcctgcagg ctagcctaag tacgtactc 29

<210> 60
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 60
aagcggccgc ggtgatgact g 21

<210> 61
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<400> 61
Thr Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys
1 5 10

<210> 62
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 62
atccgcgccg ccatccccaa gcactgctgg gtcaag 36

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<400> 63
Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
1 5 10 15

<210> 64
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (21)..(21)
<223> y = c or t

<220>
<221> unsure

<222> (33)..(33)
<223> y = c or t

<400> 64
gccctcttcg tcctcggcca ygactgcggc cayggctcgt tctcg 45

<210> 65
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (4)..(4)
<223> r = a or g

<220>
<221> unsure
<222> (10)..(10)
<223> r = a or g

<220>
<221> unsure
<222> (30)..(30)
<223> r = a or g

<220>
<221> unsure
<222> (31)..(31)
<223> r = a or g

<220>
<221> unsure
<222> (34)..(34)
<223> r = a or g

<220>
<221> unsure
<222> (38)..(38)
<223> r = a or g

<220>
<221> unsure
<222> (39)..(39)
<223> y = c or t

<220>
<221> unsure
<222> (43)..(43)
<223> r = a or g

<400> 65
gagrtggtar tgggggatct gggggaagar rtgrtggryg acrtg 45

<210> 66
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<400> 66
Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn
1 5 10 15

<210> 67
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (9)..(9)
<223> y = c or t

<220>
<221> unsure
<222> (27)..(27)
<223> y = c or t

<220>
<221> unsure
<222> (36)..(36)
<223> y = c or t

<220>
<221> unsure
<222> (39)..(39)
<223> y = c or t

<400> 67
ccctaccayg gctggcgcat ctcgcaycgc acccaycayc agaac 45

<210> 68
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (7)..(7)
<223> r = a or g

<220>
<221> unsure
<222> (10)..(10)
<223> r = a or g

<220>
<221> unsure
<222> (19)..(19)
<223> r = a or g

<220>
<221> unsure
<222> (37)..(37)
<223> r = a or g

<400> 68
gttctgrtgr tgggtccgrt gcgagatgcg ccagccrtgg taggg 45

<210> 69
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<220>
<221> UNSURE
<222> (5)..(5)
<223> Xaa = Asp or His

<220>
<221> UNSURE
<222> (7)..(7)
<223> Xaa = Asp or Tyr

<400> 69
Gly Ser His Phe Xaa Pro Xaa Ser Asp Leu Phe Val
1 5 10

<210> 70
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (13)..(13)
<223> s = c or g

<220>
<221> unsure
<222> (19)..(19)
<223> k = g or t

<400> 70
ggctcgcact tcsaccccka ctcggacctc ttcgtc 36

<210> 71
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
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<222> (18)..(18)
<223> m = a or c

<220>
<221> unsure
<222> (24)..(24)
<223> w = a or t

<400> 71
gacgaagagg tccgagtmgg ggtwgaagtg cgagcc 36

<210> 72
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<220>
<221> UNSURE
<222> (3)..(3)
<223> Xaa = Tyr or Phe

<220>
<221> UNSURE
<222> (4)..(4)
<223> Xaa = Leu or Val

<220>
<221> UNSURE
<222> (11)..(11)
<223> Xaa = Leu or Ile

<400> 72
Trp Ser Xaa Xaa Arg Gly Gly Leu Thr Thr Xaa Asp Arg
1 5 10

<210> 73
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (9)..(9)
<223> k = g or t

<220>
<221> unsure

<222> (30)..(30)
<223> w = a or t

<220>
<221> unsure
<222> (32)..(32)
<223> s = c or g

<400> 73
gcgctggakg gtggtgaggc cgccgcggaw gsacgacca 39

<210> 74
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<400> 74
His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln
1 5 10 15

<210> 75
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (13)..(13)
<223> r = a or g

<220>
<221> unsure
<222> (16)..(16)
<223> r = a or g

<220>
<221> unsure
<222> (25)..(25)
<223> r = a or g

<220>
<221> unsure
<222> (40)..(40)
<223> r = a or g

<220>
<221> unsure
<222> (43)..(43)
<223> r = a or g

<400> 75
ctgggggaag agrtgrtgga tgacrtgggt gccgatgtcr tgrtg 45

<210> 76
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<220>
<221> UNSURE
<222> (2)..(2)
<223> Xaa = Leu or Phe

<220>
<221> UNSURE
<222> (5)..(5)
<223> Xaa = Gln or Lys

<220>
<221> UNSURE
<222> (12)..(12)
<223> Xaa = Val or Ile

<400> 76
His Xaa Phe Pro Xaa Ile Pro His Tyr His Leu Xaa Glu Ala Thr
1 5 10 15

<210> 77
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> unsure
<222> (12)..(12)
<223> y = c or t

<220>
<221> unsure
<222> (16)..(16)
<223> r = a or g

<220>
<221> unsure
<222> (22)..(22)
<223> r = a or g

<220>
<221> unsure
<222> (33)..(33)
<223> k = g or t

<220>
<221> unsure
<222> (42)..(42)
<223> r = a or g

<220>
<221> unsure
<222> (43)..(43)
<223> r = a or g

<400> 77
ggtggcctcg aygagrtggt artgggggat ctkggggaag arrtg 45

<210> 78
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus peptide

<220>
<221> UNSURE
<222> (3)..(3)
<223> Xaa = Ala or Ile

<220>
<221> UNSURE
<222> (6)..(6)
<223> Xaa = Leu or Phe

<400> 78
His Val Xaa His His Xaa Phe Pro Gln Ile Pro His Tyr His Leu
1 5 10 15

<210> 79
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 79
tacgcgtacc tcacgtactc gctcg 25

<210> 80
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 80
ttcttgcacc acaacgacga agcgacg 27

<210> 81
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 81
ggagtggacg tacgtcaagg gcaac 25

<210> 82
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 82
tcaagggcaa cctctcgagc gtcgac 26

<210> 83
<211> 31
<212> DNA
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